



Substitute Form PTO-1449 (Modified)	U.S. Department of Commerce Patent and Trademark Office	Attorney's Docket No. 14937.0009	Application No. 10/562,974
Information Disclosure Statement by Applicant (Use several sheets if necessary) (37 CFR § 1.98(b))		Applicant Singh et al.	
		Filing Date July 31, 2006	Group Art Unit

U.S. Patent Documents

Examiner Initial	Desig. ID	Patent Number	Issue Date	Patentee	Class	Subclass	Filing Date If Appropriate
	AA	2002/0072887	06/13/2002	Szalma et al.			

Foreign Patent Documents or Published Foreign Patent Applications

Examiner Initial	Desig. ID	Document Number	Publication Date	Country or Patent Office	Class	Subclass	Translation	
							Yes	No
	BA							

Other Documents (include Author, Title, Date, and Place of Publication)

Examiner Initial	Desig. ID	Document
	CA	McDonald et al., "Satisfying Hydrogen Bonding Potential In Proteins," Journal of Molecular Biology, vol. 238, pp. 777-793 (1994).
	CB	Wallace et al. "LIGPLOT: A Program to Generate Schematic Diagrams of Protein-Ligand Interactions," Protein Engineering, vol. 8, pp. 127-134 (1995).
	CC	Muegge et al. "A General and Fast Scoring Function for Protein-Ligand Interactions: A Simplified Potential Approach," Journal of Medicinal Chemistry, vol. 42, pp. 791-804 (1999).
	CD	Gohlke, et al. "Knowledge-based Scoring Function to Predict Protein-Ligand Interactions," Journal of Molecular Biology, vol. 295, pp. 337-356 (2000).
	CE	Hendlich et al., "Relibase: Design and Development of a Database for Comprehensive Analysis of Protein-Ligand Interactions," Journal of Molecular Biology, vol. 326, pp. 607-620 (2003).
	CF	Guenther et al., "Utilising Structural Knowledge in Drug Design Strategies: Applications Using Relibase," Journal of Molecular Biology, vol. 326, pp. 621-636 (2003).
	CG	Wang et al., "Further Development and Validation of Empirical Scoring Functions for Structure-based Binding Affinity Prediction," Journal of Computer-Aided Molecular Design, vol. 16, pp. 11-26 (2002).
	CH	Zhang et al. "Molecular Fractionation with Conjugate Caps for Full Quantum Mechanical Calculation of Protein-Molecule Interaction Energy," Journal of Chemical Physics, vol. 119, pp. 3599-3605 (2003).
	CI	Nissink et al., "Simple Knowledge-Based Descriptors to Predict Protein-Ligand Interactions, Methodology and validation." Journal of Computer-Aided Molecular Design, vol. 14, pp. 787-803 (2000).
	CJ	Engels et al., "Smart Screening: Approaches to Efficient HTS," Current Opinion in Drug Discovery & Development, vol. 4, no. 3, pp. 275-283 (2001).
	CK	McMahon et al., "Protein Kinase Inhibitors: Structural Determinants for Target Specificity," Current Opinion in Drug Discovery & Development, vol. 1, no. 2, pp. 131-146 (1998).
	CL	Mason et al., "Library Design and Virtual Screening Using Multiple 4-point Pharmacophore Fingerprints," Pacific Symposium on Biocomputing, vol. 5, pp. 573-584 (2000).
	CM	Naumann et al., "Structural Classification of Protein Kinases Using 3D Molecular Interaction Field Analysis of Their Ligand Binding Sites: Target Family Landscapes," Journal of Medicinal Chemistry, vol. 45, p. 2366-2378 (2002).

Examiner Signature	Date Considered
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	CN	Makara, "Measuring Molecular Similarity and Diversity: Total Pharmacophore Diversity," Journal of Medicinal Chemistry, vol. 44, pp. 3563-3571 (2001).
	CO	Prusis et al., "PLS Modeling of Chimeric MS04/MSH-Peptide and MC ₁ /MC ₃ -Receptor Interactions Reveals a Novel Method for the Analysis of Ligand-Receptor Interactions," Biochimica et Biophysica Acta, vol. 1544, pp. 350-357 (2001).

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